

FIGURE 1

Nucleotide and Amino Acid Sequences of Gene X

aagccctgaa gggtcaaaag aaatcaaaaa gcaaaggcta tttttttttt tttttttttt 60
ctttcattcm ttccttcttc tgtttctttc tttcttcctt tcattttttt ttctttttta 120
agagcgagcg gctctgcggt ggcgggtttgg ggtggggcgcc gccgaggtga ggtcgtctcg 180
cctcccgccg gccggtagat tggttgtttc att atg gat gga ggg gat gat ggt 234
Met Asp Gly Gly Asp Asp Gly
1 5

aac ctt att atc aaa aag agg ttt gtg tct gag gca gaa cta gat gaa 282
Asn Leu Ile Ile Lys Lys Arg Phe Val Ser Glu Ala Glu Leu Asp Glu
10 15 20

cgg cgc aaa agg agg caa gaa gaa tgg gag aaa gtt cga aaa cct gaa 330
Arg Arg Lys Arg Arg Gln Glu Glu Trp Glu Lys Val Arg Lys Pro Glu
25 30 35

gat cca gaa gaa tgt cca gag gag gtt tat gac cct cga tct cta tat 378
Asp Pro Glu Glu Cys Pro Glu Glu Val Tyr Asp Pro Arg Ser Leu Tyr
40 45 50 55

[illegible]

gaa agg cta cag gaa cag aag gac agg aag cag cag gag tac gag gaa	426
Glu Arg Leu Gln Glu Gln Lys Asp Arg Lys Gln Gln Glu Tyr Glu Glu	
60 65 70	
cag ttc aaa ttc aaa aac atg gta aga ggc tta gat gaa gat gag acc	474
Gln Phe Lys Phe Lys Asn Met Val Arg Gly Leu Asp Glu Asp Glu Thr	
75 80 85	
aac ttc ctt gat gag gtt tct cga cag cag gaa cta ata gaa aag caa	522
Asn Phe Leu Asp Glu Val Ser Arg Gln Gln Glu Leu Ile Glu Lys Gln	
90 95 100	
cga aga gaa gaa gaa ctg aaa gaa ctg aag gaa tac aga aat aac ctc	570
Arg Arg Glu Glu Glu Leu Lys Glu Leu Lys Glu Tyr Arg Asn Asn Leu	
105 110 115	
aag aag gtt gga att tct caa gag aac aag aag gaa gtg gaa aag aaa	618
Lys Lys Val Gly Ile Ser Gln Glu Asn Lys Lys Glu Val Glu Lys Lys	
120 125 130 135	
ctg act gtg aag cct ata gaa acc aag aac aag ttc tcc cag gcg aag	666
Leu Thr Val Lys Pro Ile Glu Thr Lys Asn Lys Phe Ser Gln Ala Lys	
140 145 150	
ctg ttg gca gga gct gtg aag cat aag agc tca gag agt ggc aac agt	714
Leu Leu Ala Gly Ala Val Lys His Lys Ser Ser Glu Ser Gly Asn Ser	
155 160 165	
gtg aaa aga ctg aaa ccg gac cct gag cca gat gac aag aat caa gag	762
Val Lys Arg Leu Lys Pro Asp Pro Glu Pro Asp Asp Lys Asn Gln Glu	
170 175 180	
ccc tca tcc tgc aag tct ctc gga aac acc tcc ctg agt ggc ccc tcc	810
Pro Ser Ser Cys Lys Ser Leu Gly Asn Thr Ser Leu Ser Gly Pro Ser	
185 190 195	
atc cac tgc ccc tct gct gca gta tgt atc ggc atc ctc cca ggc ctg	858
Ile His Cys Pro Ser Ala Ala Val Cys Ile Gly Ile Leu Pro Gly Leu	
200 205 210 215	
ggc gcc tac tct ggg agc agc gac tcc gag tcc agc tca gac agc gaa	906
Gly Ala Tyr Ser Gly Ser Ser Asp Ser Glu Ser Ser Ser Asp Ser Glu	
220 225 230	
ggc acc atc aat gcc acc gga aag att gtc tcc tcc atc ttc cga acc	954
Gly Thr Ile Asn Ala Thr Gly Lys Ile Val Ser Ser Ile Phe Arg Thr	
235 240 245	

tcccccaaggg tagatcggac cgttcacgct gcctataggc attatgtccc tcaaaaaaaaa 1065
actcctttgc ctgcatcctg tgtacaacat gacattttta accaatccaa tctaaaaatg 1125
tgccagaatc cacctgtggc ccgaatcgtg ttgggttcct ctttctactc cactgcagat 1185
gaccaaacct gtcccgtgc cactttctc actgatattg ggaggagggc aaggcccagc 1245
cgaagtcca ctaaaaatgc ccaggagaa taggcaccgg ctggcttgcc aaagggtttg 1305
ggttttattg ctttctgtt tttctttcc cgacagcaca aagaagtaag ggcagttatt 1365
ggacaggtgt tatttaaaca ttctattgta aatgaatgtg ttgtttgggt ctactgcatt 1425
gtggagcatg cgggggaaga gaactgacct aggtaatgaa atggagccct tccctggaac 1485
taaccagtcc ttgatgttg gtgactaagt aaagatgata aacccatct gctgggggtg 1545
tcacttcaca ctggcatgc attgtgaaag cttcccatc ccttgccat tccctctctc 1605
ctctctctcc aacccatct atgcaggaag ggactgctaa caagaacgt tccatctcaa 1665
acctttctc tgcctgggaa attattttat gtttgtttt gaaataaagg atttagttta 1725
agattctaaa ttttagagaa acaaacgtag gccttggtta ctaatagcca gacatcagaa 1785
ctgcaggtag gtatgttaat gagatgactt attctggca gctcctggaa tcctaattt 1845
gtaaatgagt gggacacact tgcattattg gaccattcta ttgaggccct ctctgtttaa 1905
tgcattatt acttgtgctt ttaactgtg aactatttc taacctaaag gtgctgccct 1965
agtacttttc tttgtgcct ctgtgtctt tttccttcc caaacagcaa ctctgaggcc 2025
atgagcagcc aaaaactaga ggtactgtc cactcgtct cataaaggga aacgggctca 2085
tcccttggat tctggaggag ggagagggag atgggtgtga ggcctcgagg acagagatag 2145
acatgagctt tgacaacaat ctgtaggctc tctgtctta gaataagcat gtaccattct 2205
ttatccatc cccttatcc tacatcaat gtttttactt tcttgggtgt gagactgagt 2265
gagacacaca caaatgtgt tgacactgt atgcccgcag gcagagcagc tactgacttt 2325

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2850

Nucleotide and Amino Acid Sequences of Plasmolipin Like Protein (PLP)

acggcggccg tagcgacctc gggaggcaag cggagccgcc atg gcc gag ttc ccg 115
Met Ala Glu Phe Pro
1 5

tcg aaa gtt agc acg cgg acc agc agt cct gcg cag ggc gcc gaa gcc 163
Ser Lys Val Ser Thr Arg Thr Ser Ser Pro Ala Gln Gly Ala Glu Ala
10 15 20

tcg gtg tcg gcg ctg cgc ccg gac ctg ggc ttc gtg cgc tcc cgc ctc 211
Ser Val Ser Ala Leu Arg Pro Asp Leu Gly Phe Val Arg Ser Arg Leu

[illegible]

[illegible]

25	30	35	
ggg gcg ctc atg ctg ctg cag ctg gtg ctg ggg ctg ctg gtg tgg gcg	259		
Gly Ala Leu Met Leu Leu Gln Leu Val Leu Gly Leu Leu Val Trp Ala			
40 45 50			
ctg att gcg gac acc ccg tac cac ctg tat ccg gcc tat ggc tgg gtg	307		
Leu Ile Ala Asp Thr Pro Tyr His Leu Tyr Pro Ala Tyr Gly Trp Val			
55 60 65			
atg ttc gtc gct gtc ttc ctc tgg ctg gtg aca atc gtc ctc ttc aac	355		
Met Phe Val Ala Val Phe Leu Trp Leu Val Thr Ile Val Leu Phe Asn			
70 75 80 85			
ctc tac ctg ttt cag ctg cac atg aag ttg tac atg gtt ccc tgg cca	403		
Leu Tyr Leu Phe Gln Leu His Met Lys Leu Tyr Met Val Pro Trp Pro			
90 95 100			
ctg gtg tta atg atc ttt aac atc agc gcc acc gtt ctc tac atc acc	451		
Leu Val Leu Met Ile Phe Asn Ile Ser Ala Thr Val Leu Tyr Ile Thr			
105 110 115			
gcc ttc atc gcc tgc tct gcg gca gtt gac ctg aca tcc ctg agg ggc	499		
Ala Phe Ile Ala Cys Ser Ala Ala Val Asp Leu Thr Ser Leu Arg Gly			
120 125 130			
acc cgg cct tat aac cag cgc gcg gct gcc tcg ttc ttt gcg tgt ttg	547		
Thr Arg Pro Tyr Asn Gln Arg Ala Ala Ala Ser Phe Phe Ala Cys Leu			
135 140 145			
gtg atg atc gcc tat gga gtg agt gcc ttc ttc agc tac cag gcc tgg	595		
Val Met Ile Ala Tyr Gly Val Ser Ala Phe Phe Ser Tyr Gln Ala Trp			
150 155 160 165			
cga gga gta ggc agc aat gcg gcc acc agt cag atg gct ggc ggc tat	643		
Arg Gly Val Gly Ser Asn Ala Ala Thr Ser Gln Met Ala Gly Gly Tyr			
170 175 180			
gcc taa acc acc tgt gcc acg gcc ccc tct ggg gct gaa gcc gcc gct	691		
Ala Thr Thr Cys Ala Thr Ala Pro Ser Gly Ala Glu Ala Ala Ala			
185 190 195			
ggg tca cag agc agg gtc acc ctg caa gcc tga agc tgg gga gcc ctg	739		
Gly Ser Gln Ser Arg Val Thr Leu Gln Ala Ser Trp Gly Ala Leu			
200 205 210			
cgt gga gtc agc cca acagggactg catttgctcc tctctgcccg tcagacataa	794		
Arg Gly Val Ser Pro			

1516

FIGURE 3

Nucleotide and Amino Acid Sequences of ORPH-PPAR (PPAR)

gtgctgtgag gggcttcggg accttggggc agctcctgag ttcagacaga gttcaggaag 60
ggagacaggg gcacagagag acagaggttc atggactgag gcaaaggctg ggccaggctc 120
agcaaccag gcctcccgca ggcaggcaga ggctgccctg taaccc atg gag acc 175
Met Glu Thr
1
aga cca aca gct ctg atg agc tcc aca gtg gct gca gct gcg cct gca 223
Arg Pro Thr Ala Leu Met Ser Ser Thr Val Ala Ala Ala Ala Pro Ala
5 10 15
gct ggg gct gcc tcc agg aag gag tct cca ggc aga tgg ggc ctg ggg 271
Ala Gly Ala Ala Ser Arg Lys Glu Ser Pro Gly Arg Trp Gly Leu Gly
20 25 30 35
gag gat ccc aca ggc gtg agc ccc tcg ctc cag tgc cgc gtg tgc gga 319
Glu Asp Pro Thr Gly Val Ser Pro Ser Leu Gln Cys Arg Val Cys Gly
40 45 50
gac agc agc agc ggg aag cac tat ggc atc tat gcc tgc aac ggc tgc 367
Asp Ser Ser Ser Gly Lys His Tyr Gly Ile Tyr Ala Cys Asn Gly Cys
55 60 65
agc ggc ttg ttc aag agg agc gta cgg cgg agg ctc atc tac agg tgc 415
Ser Gly Phe Phe Lys Arg Ser Val Arg Arg Arg Leu Ile Tyr Arg Cys
70 75 80
cag gtg ggg gca ggg atg tgc ccc gtg gac aag gcc cac cgc aac cag 463
Gln Val Gly Ala Gly Met Cys Pro Val Asp Lys Ala His Arg Asn Gln
85 90 95
tgc cag gcc tgc cgg ctg aag aag tgc ctg cag gcg ggg atg aac cag 511
Cys Gln Ala Cys Arg Leu Lys Lys Cys Leu Gln Ala Gly Met Asn Gln
100 105 110 115
gac gcc gtg cag aac gag cgc cag ccg cga agc aca gcc cag gtc cac 559
Asp Ala Val Gln Asn Glu Arg Gln Pro Arg Ser Thr Ala Gln Val His
120 125 130

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ctg gac agc atg gag tcc aac act gag tcc cgg ccg gag tcc ctg gtg 607
Leu Asp Ser Met Glu Ser Asn Thr Glu Ser Arg Pro Glu Ser Leu Val
135 140 145

gct ccc ccg gcc ccg gca ggg cgc agc cca cgg ggc ccc aca ccc atg 655
 Ala Pro Pro Ala Pro Ala Gly Arg Ser Pro Arg Gly Pro Thr Pro Met
 150 155 160

tct gca gcc aga gcc ctg ggc cac cac ttc atg gcc agc ctt ata aca 703
Ser Ala Ala Arg Ala Leu Gly His His Phe Met Ala Ser Leu Ile Thr
165 170 175

gct gaa acc tgt gct aag ctg gag cca gag gat gct gat gag aat att 751
Ala Glu Thr Cys Ala Lys Leu Glu Pro Glu Asp Ala Asp Glu Asn Ile
180 185 190 195

gat gtc acc agc aat gac cct gag ttc ccc tcc tct cca tac tcc tct 799
Asp Val Thr Ser Asn Asp Pro Glu Phe Pro Ser Ser Pro Tyr Ser Ser
200 205 210

tcc tcc ccc tgc ggc ctg gac agc atc cat gag acc tcg gct cgc cta 847
Ser Ser Pro Cys Gly Leu Asp Ser Ile His Glu Thr Ser Ala Arg Leu
215 220 225

ctc ttc atg gcc gtc aag tgg gcc aag aac ctg cct gtg ttc tcc agc 895
Leu Phe Met Ala Val Lys Trp Ala Lys Asn Leu Pro Val Phe Ser Ser
230 235 240

ctg ccc ttc cgg gat cag gta cct acc ggc ctg cct gct ggg gag cta 943
Leu Pro Phe Arg Asp Gln Val Pro Thr Gly Leu Pro Ala Gly Glu Leu
245 250 255

ggc tgg gct ggg gtc agg cgg ccc act cga gtc aac cag aca ggg cac 991
Gly Trp Ala, Gly Val Arg Arg Pro Thr Arg Val Asn Gln Thr Gly His
260 265 270 275

aca cat ccc cac gcc agt atg aat gca cac agc ttg gat ggt gat ggc 1039
Thr His Pro His Ala Ser Met Asn Ala His Ser Leu Asp Gly Asp Gly
280 285 290

tgg gga cac aca tac ctc tgattcagcg atggctgggg tgcattctcag 1087
Trp Gly His Thr Tyr Leu
295

ggatggtgac ggtgggggtg catgcatctc tggcacaggg atgatggtcg ggggtgcacac 1147

ctaggagatg atgatggcta gggacctaca gggccaggg tcttcttaag ttctggaaga 1207

[illegible]

2177

NT2 Like Protein (NTPL) Gene
Fragment Sequence

ACTGNCAGGAACCTCTGCCACCGCCACCGGCTCCCATGGCCCATACCCAGTGGGGGTGCCCCAGCAGCGGGGGCAGCC
CCCATGGGCCCCCAGTATTGCGTGTGCAAGGTGGAGCTGTGAGTGAGTGGCCAGAACCTACTGGACCGGGATGTTACCTC
CAAGTCCGACCCCTTCTGTGTCCTCTTTACAGAGAACAATGGCAGATGGATCGAG

[illegible]

[illegible]

GAATTCACACAAAGGAGTCCAGGGTCTCGCTCTGTACACAGGCTGGAGTGC
AGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCC
TCATGCCTCAGCCTCCCGAGT.AGCTGGGATTACAGGTGGTGA CTCTCCAAGAG
TGA CTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGT
TCCTGCTGAGTCTGCTCTTCTGCTCCAAGCCAGCGGAACCAGACACACAGG
AGCAGCCTCCACTACAAACCCACACCAGACCTGCGCATCTCCATCGAGA ACT
CCGAAGAGGCCCTCACAGTCCATGCCCCCTTCCCTGCAGCCCACCCTGCTTCC
CGATCCTTCCCTGACCCCAGGGGGCCTCTACCACTTCTGCCTCTACTGGAACCG
ACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGA CTCTTGTCTGAGTG
ACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCA
GGGCCCCCGCTGTTAGCC.ACTTCTGTCACTCTCTGGTGGAGCCCTCAGAACA
TCAGCCTGCCCAGTGCCGCCAGCTTCACTTCTCCTTCCACAGTCTCCCCAC
ACGGCCGCTCAC.AATGCCTCGGTGGACATGTGCGAGCTCAA.AGGGACCTCC
AGCTGCTCAGCCAGTTCTTG.AAGC.ATCCCCAGAAGGCCTCAAGGAGGCCCTC
GGCTGCCCCCGCCAGCCAGC.AGTTGCAGAGCCTGGAGTCGAA.ACTGACCTCT
GTGAGATTCA.TGGGGGACATGGTGTCTTTCGAGGAGGACCGGATCA.AACGCCA
CGGTGTGGA.AGCTCC.AGCCC.ACAGCCGGCCTCCAGGACCTGCACATCCACTC
CCGGCAGGAGGAGGAGCAGAGCGAGATCATGGAGT.ACTCGGTGCTGCTGCCT
CGA.ACACTCTTCC.AGAGGACGA.AAGGCCGGAGGGGGGAGGCTGAGAAGAGA
CTCCTCCTGGTGGACTTCA.GCAGCCA.AGCCCTGTTCCAGGACAAGAATTCCA
GCCACGTCCTGGGTGAGA.AGGTCTTGGGGATTGTGGTACAGAACACCAAAGT
AGCCA.ACCTCACGGAGCCCGTGGTGTCTACCTTCCAGCACCAGCTACAGCCG
AAGA.ATGTGACTCTGCA.AATGTGTGTTCTGGGTTGA.AGACCCACATTGAGCA
GCCCCGGGGCATTGG.AGCAGTGCTGGGTGTGAGACCGTCAAGGAGAGAA.ACCC
AA.ACATCCTGCTTCTGCA.ACC.ACTTGACCT.ACTTTGCAGTGCTGATGGTCTCC
TCGGTGGAGGTGGACGCCGTGC.AAAGC.ACTACCTGAGCCTCCTCTCCTACG
TGGGCTGTGTCTCTCTGCCCTGGCCTGCCTTGTCA.CCATTGCCGCCTACCTCT
GCTCCAGGAGGA.AACCTCGGG.ACTACACCATCAAGGTGCACATGAACCTGCT
GCTGGCCGTCTTCTCTGCTGGAC.ACGAGCTTCTGCTCAGCGAGCCGGTGGCCC
TGAC.AGGCTCTG.AGGCTGGCTGCCGAGCCAGTGCC.ATCTTCTGCACTTCTCC
CTGCTCACTTGCCTTTCTCTGGATGGGCCTCG.AGGGGTACA.ACCTCTACCGACT
CGTGGTGGAGGTCTTTGGC.ACCTATGTCCCTGGCTACCT.ACTCAAGCTGAGCG
CC.ATGGGCTGGGGCTTCCCC.ATCTTCTGGTGACGCTGGTGGCCCTGGTGGAT
GTGGACA.ACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCG
TCATCT.ACCCTTCC.ATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACC
AACCTGGGCCTCTTCA.GCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCAC
CATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAAAAGTGGTCACAT
GTGCTGAC.ACTGCTGGGCCTCA.GCCTGGTCTTGGCCTGCCCTGGGCCTTGAT
CTTCTTCTCCTTTGCTTCTGGCACCTTCCAGCTTGTCTCTCTCTA.CCTTTTCAG
CATCATCACTCCTTCCA.AAGGCTTCTCATCTTTCATCTGGT.ACTGGTCCATGC

GGCTGCAGGCCCGGGGTGGCCCTCCCCTCTGAAGAGCAACTCAGACAGCGC
 CAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCC
 AGCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCC
 TGTGGCCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGA
 AAGCCCAACGACCATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCC
 GGCTGGGCTTTTGAATTGGCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCA
 CGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTGTCCCCACATCTG
 TCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTGGGGCCAGCCCT
 CATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATCCT
 GTGCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTC
 ACCCTGAGGGCACTCTGCATCCTCTGTCAATTTAACCTCAGGTGGCACCCAGG
 GCGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGA
 GGCCCTTTGCCAGGAGCACAGCAGCAGCTCGCCTACCTCTGAGCCCAGGCCC
 CCTCCCTCCCTCAGCCCCCAGTCCTCCCTCCATCTTCCCTGGGGTTCTCCTCC
 TCTCCAGGGCCTCCTTGCTCCTTCGTTACAGCTGGGGGTCCCCGATTCCAA
 TGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATG
 TTTGTCTACTGCACAAGCCTCGGCCTGCCCCTGAGCCAGGCTCGGTACCGATG
 CGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATT
 GCCCTTGCTCACCCCTGACCAAGCACACGCCTCAGAGGGGGCCCTCAGCCTCTC
 CTGAAGCCCTCTTGTGGCAAGAAGTGTGGACCATGCCAGTCCCGTCTGGTTTC
 CATCCCACCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA
 GAGCCTGACACTCTCCTAAGAGGTTCTCTCAAGCCCCCAAATAGCTCCAGG
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 CTTCTGACAGGAGTCAGCGTTCAATCTTGACCTTGAAGATGGGAAGGATGTTT
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 TGTAGAGAATTTGGAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATC
 AGCTGTTGTAAATCGCCTARCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAATAAAAAAAAAAAAAA

protein

MCELKRDQLLSQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFE
 EDRINATVWKLQPTAGLQDLHIHSRQEEQSEIMEYSVLLPRTLFRQTKGRRGEA
 EKRLLLVDFSSQALFQDKNSSHVLGEKVLGIVVQNTKVANLTEPVVLTFFQHQLQ
 PKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRETQTSFCNHLTYFAVLMVSS
 VEVDVAVHKHYLSLLSYVGCVVSAALCLVTIAAYLCSRRKPRDYTIKVMNLLLA
 VFLLDTSFLLSEPVALTGSEAGCRASAFHFSLTCLSWMGLEGYNLYRLVVEV
 FGTYVPGYLLKLSAMGWGFIFLVTLVALVDVDNYGPILA VHRTPGVIYPSMC
 WIRDSLVSYTNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSL
 VLGLPWALIFFSFASGTFQLVVL YLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKS
 NSDSARLPISSGSTSSRI